



SEQUENCE LISTING

<110> DERBRAH, KNUTZON
WIKERJI, PRADIP
HUANG, YUNG-SHENG
THURMOND, JENNIFER
CHAUDHARY, SUNITA
LEONARD, AMANDA

<120> Methods and Compositions for Synthesis of Long Chain
Polyunsaturated Fatty Acids

<130> CGAB-210 USA

<140> US 09/367,013

<141> 1999-08-05

<150> US 08/834,655

<151> 1997-04-11

<160> 40

<170> PatentIn version 3.0

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<212> DNA

<213> Mortierella alpina

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<221> misc_feature

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<223> Description of Combined DNA/RNA Molecule: Delta-6 Desaturase
Nucleic Acid Sequence

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Phe	Pro	Ser	Met	Pro	Arg	His	Asn	Phe	Ser	Lys	Ile	Gln	Pro	Ala	Val
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Glu	Thr	Leu	Cys	Lys	Lys	Tyr	Asn	Val	Arg	Tyr	His	Thr	Thr	Gly	Met
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Glu Glu Leu Thr Arg	Met Trp Ser Arg Phe	Met Val Leu Asn Gln Thr		
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Trp Phe Tyr Phe Pro	Ile Leu Ser Phe Ala	Arg Leu Ser Trp Cys Leu		
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Tyr	Asn	Val	Arg	Tyr	His	Thr	Thr	Gly	Met	Ile	Glu	Gly	Thr	Ala	Glu
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 <222> (1)..(104)
 <223> Amino acids 27, 48, and 63 uncertain of sequence

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Lys	Trp	Thr	His	Asn	Ala	His	His	Leu	Ala	Cys	Asn	Ser	Leu	Asp	Tyr
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Gly	His	Asp	Ser	Gly	His	Tyr	Val	Ile	Met	Ser	Asn	Lys	Ser	Tyr	Asn
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Leu	Asp	Tyr	Asp	Pro	Asp	Leu	Gln	His	Ile	Pro	Val	Phe	Ala	Val	Ser
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Thr	Lys	Phe	Phe	Ser	Ser	Leu	Thr	Ser	Arg	Phe	Tyr	Asp	Arg	Lys	Leu
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Tyr	Tyr	Pro	Val	Asn	Cys	Phe	Gly	Arg	Ile	Asn	Leu	Phe	Ile	Gln	Thr
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Phe	Ala	Gly	Ile	Leu	Val	Phe	Trp	Thr	Trp	Phe	Pro	Leu	Leu	Val	Ser
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Cys	Leu	Pro	Asn	Trp	Pro	Glu	Arg	Phe	Phe	Phe	Val	Phe	Thr	Ser	Phe
			180					185					190		
Thr	Val	Thr	Ala	Leu	Gln	His	Ile	Gln	Phe	Thr	Leu	Asn	His	Phe	Ala
		195					200					205			
Ala	Asp	Val	Tyr	Val	Gly	Pro	Pro	Thr	Gly	Ser	Asp	Trp	Phe	Glu	Lys
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Gln	Ala	Ala	Gly	Thr	Ile	Asp	Ile	Ser	Cys	Arg	Ser	Tyr	Met	Asp	Trp
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 <223> Amino acids 2, 3, 30, 121, and 125 uncertain of sequence.

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Phe	Thr	Gly	Phe	Thr	Val	Thr	Ala	Leu	Gln	His	Ile	Gln	Phe	Thr	Leu
		35					40					45			
Asn	His	Phe	Ala	Ala	Asp	Val	Tyr	Val	Gly	Pro	Pro	Thr	Gly	Ser	Asp
	50					55					60				
Trp	Phe	Glu	Lys	Gln	Ala	Ala	Gly	Thr	Ile	Asp	Ile	Ser	Cys	Arg	Ser
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Tyr	Met	Asp	Trp	Phe	Phe	Cys	Gly	Leu	Gln	Phe	Gln	Leu	Glu	His	His
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Leu	Phe	Pro	Arg	Leu	Pro	Arg	Cys	His	Leu	Arg	Lys	Val	Ser	Pro	Val
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Gly	Gln	Arg	Gly	Phe	Gln	Arg	Lys	Xaa	Asn	Leu	Ser	Xaa			
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 <213> Homo sapiens

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 <223> Amino acid at 110 uncertain of sequence

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			20					25					30		
Gly	Leu	Phe	Phe	Ile	Val	Arg	Phe	Leu	Glu	Ser	Asn	Trp	Phe	Val	Trp
		35					40					45			

Val Thr Gln Met Asn His Ile Pro Met His Ile Asp His Asp Arg Asn
50 55 60

Met Asp Trp Val Ser Thr Gln Leu Gln Ala Thr Cys Asn Val His Lys
65 70 75 80

Ser Ala Phe Asn Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile Glu
85 90 95

His His Leu Phe Pro Thr Met Pro Arg His Asn Tyr His Xaa Val Ala
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Pro Leu Val Gln Ser Leu Cys Ala Lys His Gly Ile Glu Tyr Gln Ser
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Lys Pro Leu
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<210> 10

<211> 87

<212> PRT

<213> Caenorhabditis elegans

<400> 10

Cys Ser Pro Lys Ser Ser Pro Thr Arg Asn Met Thr Pro Ser Pro Phe
1 5 10 15

Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln Ile Glu His His Leu
20 25 30

Phe Pro Thr Met Pro Arg Cys Asn Leu Asn Arg Cys Met Lys Tyr Val
35 40 45

Lys Glu Trp Cys Ala Glu Asn Asn Leu Pro Tyr Leu Val Asp Asp Tyr
50 55 60

Phe Val Gly Tyr Asn Leu Asn Leu Gln Gln Leu Lys Asn Met Ala Glu
65 70 75 80

Leu Val Gln Ala Lys Ala Ala
85

<210> 11

<211> 143

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> (1)..(143)

<223> Amino acid 125 uncertain of sequence

<400> 11

Arg His Glu Ala Ala Arg Gly Gly Thr Arg Leu Ala Tyr Met Leu Val
1 5 10 15

Cys Met Gln Trp Thr Asp Leu Leu Trp Ala Ala Ser Phe Tyr Ser Arg
20 25 30

Phe Phe Leu Ser Tyr Ser Pro Phe Tyr Gly Ala Thr Gly Thr Leu Leu
 35 40 45
 Leu Phe Val Ala Val Arg Val Leu Glu Ser His Trp Phe Val Trp Ile
 50 55 60
 Thr Gln Met Asn His Ile Pro Lys Glu Ile Gly His Glu Lys His Arg
 65 70 75 80
 Asp Trp Ala Ser Ser Gln Leu Ala Ala Thr Cys Asn Val Glu Pro Ser
 85 90 95
 Leu Phe Ile Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile Glu His
 100 105 110
 His Leu Phe Pro Thr Met Thr Arg His Asn Tyr Arg Xaa Val Ala Pro
 115 120 125
 Leu Val Lys Ala Phe Cys Ala Lys His Gly Leu His Tyr Glu Val
 130 135 140

<210> 12
 <211> 35
 <212> DNA
 <213> Artificial/Unknown

 <220>
 <221> misc_feature
 <222> ()..()
 <223> Description of Artificial Sequence: PCR Primer

<400> 12
 ccaagcttct gcaggagctc tttttttttt ttttt

35

<210> 13
 <211> 33
 <212> DNA
 <213> Artificial/Unknown

 <220>
 <221> misc_feature
 <222> ()..()
 <223> Description of Combined RNA/DNA Molecule:PCR Primer

<400> 13
 cuacuacuac uaggagtctt ctacggtggt ttg

33

<210> 14
 <211> 33
 <212> DNA
 <213> Artificial/Unknown

 <220>
 <221> misc_feature
 <222> ()..()
 <223> Description of Combined RNA/DNA Molecule:PCR Primer

<400> 14
caucaucauc auatgatgct caagctgaaa ctg 33

<210> 15
<211> 39
<212> DNA
<213> Artificial/Unknown

<220>
<221> misc_feature
<222> ()..()
<223> Description of Artificial Sequence: PCR Primer

<400> 15
taccaactcg agaaaatggc tgctgctccc agtgtgagg 39

<210> 16
<211> 39
<212> DNA
<213> Artificial/Unknown

<220>
<221> misc_feature
<222> ()..()
<223> Description of Artificial Sequence:PCR Primer

<400> 16
aactgatcta gattactgcg ccttacccat cttggaggc 39

<210> 17
<211> 39
<212> DNA
<213> Artificial/Unknown

<220>
<221> misc_feature
<222> ()..()
<223> Description of Artificial Sequence:PCR Primer

<400> 17
taccaactcg agaaaatggc acctcccaac actatcgat 39

<210> 18
<211> 39
<212> DNA
<213> Artificial/Unknown

<220>
<221> misc_feature
<222> ()..()
<223> Description of Artificial Sequence:PCR Primer

<400> 18
aactgatcta gattacttct tgaaaaagac cacgtctcc

39

<210> 19
<211> 746
<212> DNA
<213> Dictyostelium discoideum

<400> 19
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cactcctcta tggattttac aactcctca atcgactca agattgggaa gcttttgtaa 120
aggatggtaa aaatgggtgca attcgtgtta gtgtcgccac aaatttcgat aaggccgctt 180
acgtcattgg taaattgtct tttgttttct tccgtttcat cttccactc cgttatcata 240
gctttacaga tttaatttgt ttttccctca ttgctgaatt cgtcttttgg tggatatctca 300
caattaattt ccaagttagt catgtcgctg aagatctcaa attctttgct acccctgaaa 360
gaccagatga accatctcaa atcaatgaag attgggcaat cttcaactt aaaactactc 420
aagattatgg tcatgggtca ctcttttgta ctttttttag tggttcttta aatcatcaag 480
ttgttcatca tttattccca tcaattgctc aagatttcta ccacaaactt gtaccaattg 540
taaaagaagt ttgtaaagaa cataacatta cttaccacat taaaccaaac ttcactgaag 600
ctattatgtc acacattaat tacctttaca aaatgggtaa tgatccagat tatgttaaaa 660
aaccattagc ctcaaaagat gattaaatga aataacttaa aaaccaatta tttacttttg 720
acaaacagta atattaataa atacaa 746

<210> 20
<211> 228
<212> PRT
<213> Dictyostelium discoideum

<220>
<221> UNSURE
<222> (1)..(228)
<223> Amino acid 228 uncertain of sequence

<400> 20

Tyr Val Thr Pro Phe Gln Thr Arg Ser Trp Tyr His Lys Tyr Gln His
1 5 10 15

Ile Tyr Ala Pro Leu Leu Tyr Gly Ile Tyr Thr Leu Lys Tyr Arg Thr
20 25 30

Gln Asp Trp Glu Ala Phe Val Lys Asp Gly Lys Asn Gly Ala Ile Arg
35 40 45

Val Ser Val Ala Thr Asn Phe Asp Lys Ala Ala Tyr Val Ile Gly Lys

50	55	60
Leu Ser Phe Val Phe Phe Arg Phe Ile Leu Pro Leu Arg Tyr His Ser		
65	70	75 80
Phe Thr Asp Leu Ile Cys Tyr Phe Leu Ile Ala Glu Phe Val Phe Gly		
	85	90 95
Trp Tyr Leu Thr Ile Asn Phe Gln Val Ser His Val Ala Glu Asp Leu		
	100	105 110
Lys Phe Phe Ala Thr Pro Glu Arg Pro Asp Glu Pro Ser Gln Ile Asn		
	115	120 125
Glu Asp Trp Ala Ile Leu Gln Leu Lys Thr Thr Gln Asp Tyr Gly His		
	130	135 140
Gly Ser Leu Leu Cys Thr Phe Phe Ser Gly Ser Leu Asn His Gln Val		
145	150	155 160
Val His His Leu Phe Pro Ser Ile Ala Gln Asp Phe Tyr Pro Gln Leu		
	165	170 175
Val Pro Ile Val Lys Glu Val Cys Lys Glu His Asn Ile Thr Tyr His		
	180	185 190
Ile Lys Pro Asn Phe Thr Glu Ala Ile Met Ser His Ile Asn Tyr Leu		
	195	200 205
Tyr Lys Met Gly Asn Asp Pro Asp Tyr Val Lys Lys Pro Leu Ala Ser		
	210	215 220
Lys Asp Asp Xaa		
225		

<210> 21
 <211> 494
 <212> DNA
 <213> *Phaeodactylum tricornutum*

 <220>
 <221> misc_feature
 <222> ()..()
 <223> n at positions 11,20,29,31,40,53,453,489 may be a, c, g, or t

<400> 21	
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cccccaagc cttttgtcga ctggttctgt ggtggcttcc agtaccaagt cgaccaccac	120
ttattcccca gcctgccccg acacaatctg gccaaagacac acgcactggg cgaatcgttc	180
tgcaaggagt ggggtgtcca gtaccacgaa gccgacctcg tggacgggac catggaagtc	240
ttgcaccatt tgggcagcgt ggccggcgaa ttcgtcgtgg attttgtacg cgacggaccc	300
gccatgtaat cgtcgttcgt gacgatgcaa gggttcacgc acatctacac aactcactc	360
acacaactag tgtaactcgt atagaattcg gtgtcgacct ggaccttggt tgactgggtg	420

gggatagggt aggtaggcgg acgcgtgggt cgnccccggg aattctgtga ccggtacctg 480
gccccgcgtna aagt 494

<210> 22
<211> 102
<212> PRT
<213> Phaeodactylum tricornutum

<220>
<221> UNSURE
<222> (1)..(102)
<223> Amino acids 4,7,10,11,14, and 18 uncertain of sequence

<400> 22

Phe Trp Lys Xaa Pro Ser Xaa Pro Arg Xaa Xaa Gln Val Xaa Gly Ala
1 5 10 15
Glu Xaa Gly Phe Pro Pro Lys Pro Phe Val Asp Trp Phe Cys Gly Gly
20 25 30
Phe Gln Tyr Gln Val Asp His His Leu Phe Pro Ser Leu Pro Arg His
35 40 45
Asn Leu Ala Lys Thr His Ala Leu Val Glu Ser Phe Cys Lys Glu Trp
50 55 60
Gly Val Gln Tyr His Glu Ala Asp Leu Val Asp Gly Thr Met Glu Val
65 70 75 80
Leu His His Leu Gly Ser Val Ala Gly Glu Phe Val Val Asp Phe Val
85 90 95
Arg Asp Gly Pro Ala Met
100

<210> 23
<211> 520
<212> DNA
<213> Artificial/Unknown

<220>
<221> misc_feature
<222> ()..()
<223> Description of Artificial Sequence:Schizochytrium cDNA Clone

<400> 23
ggatggagtt cgtctggatc gctgtgcgct acgcgacgtg gtttaagcgt catgggtgcg 60
cttgggtaca cgccggggca gtcgttgggc atgtacttgt gcgcctttgg tctcggtgc 120
atttacattt ttctgcagtt cgccgtaagt cacaccatt tgcccgtag caaccggag 180
gatcagctgc attggctcga gtacgcgcgg accacactgt gaacatcagc accaagtcgt 240
ggtttgtcac atggtggatg tcgaacctca actttcagat cgagcaccac cttttcccca 300

cggcgccccca gttccgtttc aaggagatca gcccgcgcggt cgaggccctc ttcaagcgcc 360
acgggtctccc ttactacgac atgccctaca cgagcgccgt ctccaccacc ttgccaacc 420
tctactccgt cgccattcc gtcggcgacg ccaagcgga ctagcctctt ttcctagacc 480
ttaattcccc accccacccc atgttctgtc ttcctccgc 520

<210> 24
<211> 153
<212> PRT
<213> Artificial/Unknown
<220>
<221> misc_feature
<222> ()..()
<223> Description of Artificial Sequence:Schizochytrium cDNA Clone

<400> 24

Met Glu Phe Val Trp Ile Ala Val Arg Tyr Ala Thr Trp Phe Lys Arg
1 5 10 15
His Gly Cys Ala Trp Val His Ala Gly Ala Val Val Gly His Val Leu
20 25 30
Val Arg Leu Trp Ser Arg Leu His Leu His Phe Ser Ala Val Arg Arg
35 40 45
Lys Ser His Pro Phe Ala Arg Glu Gln Pro Gly Gly Ser Ala Ala Leu
50 55 60
Ala Arg Val Arg Ala Asp His Thr Val Asn Ile Ser Thr Lys Ser Trp
65 70 75 80
Phe Val Thr Trp Trp Met Ser Asn Leu Asn Phe Gln Ile Glu His His
85 90 95
Leu Phe Pro Thr Ala Pro Gln Phe Arg Phe Lys Glu Ile Ser Pro Arg
100 105 110
Val Glu Ala Leu Phe Lys Arg His Gly Leu Pro Tyr Tyr Asp Met Pro
115 120 125
Tyr Thr Ser Ala Val Ser Thr Thr Phe Ala Asn Leu Tyr Ser Val Gly
130 135 140
His Ser Val Gly Asp Ala Lys Arg Asp
145 150

<210> 25
<211> 420
<212> DNA
<213> Artificial/Unknown
<220>
<221> misc_feature
<222> ()..()
<223> Description of Artificial Sequence:Schizochytrium cDNA Clone

<400> 25
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gctcccgcac atgacgtacc gcgtggtcga gattgttggt ctcttcgtgc tttccttttg 120
gctgatgggt cagtcttcac cctcgcgct cgctctcggc attgtcgtca gcggcatctc 180
tcagggtcgc tgcggctggg taatgcatga gatgggccat gggtcgttca ctggtgtcat 240
ttggcttgac gaccggttgt gcgagttctt ttacggcggt ggttgtggca tgagcgggtca 300
ttactggaaa aaccagcaca gcaaacacca cgcagcgcca aaccggctcg agcacgatgt 360
agatctcaac accttgccat tgggtggcctt caacgagcgc gtcgtgcgca aggtccgacc 420

<210> 26
<211> 140
<212> PRT
<213> Artificial/Unknown
<220>
<221> misc_feature
<222> ()..()
<223> Description of Artificial Sequence:Schizochytrium cDNA Clone

<400> 26
Arg Val Arg Pro Arg Val Arg Arg Glu Gln Leu Ile Lys Glu Gly Tyr
1 5 10 15
Phe Asp Pro Ser Leu Pro His Met Thr Tyr Arg Val Val Glu Ile Val
20 25 30
Val Leu Phe Val Leu Ser Phe Trp Leu Met Gly Gln Ser Ser Pro Leu
35 40 45
Ala Leu Ala Leu Gly Ile Val Val Ser Gly Ile Ser Gln Gly Arg Cys
50 55 60
Gly Trp Val Met His Glu Met Gly His Gly Ser Phe Thr Gly Val Ile
65 70 75 80
Trp Leu Asp Asp Arg Leu Cys Glu Phe Phe Tyr Gly Val Gly Cys Gly
85 90 95
Met Ser Gly His Tyr Trp Lys Asn Gln His Ser Lys His His Ala Ala
100 105 110
Pro Asn Arg Leu Glu His Asp Val Asp Leu Asn Thr Leu Pro Leu Val
115 120 125
Ala Phe Asn Glu Arg Val Val Arg Lys Val Arg Pro
130 135 140

<210> 27
<211> 1219
<212> DNA

<213> Homo sapiens

<400> 27

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gcacgccgac cggcgccggg agatcctggc aaagtatcca gagataaagt ccttgatgaa      60
acctgatccc aatttgatat ggattataat tatgatgggt ctcacccagt tgggtgcatt      120
ttacatagta aaagacttgg actggaaatg ggtcatatgt ggggcctatg cgtttggcag      180
ttgcattaac cactcaatga ctctggctat tcatgagatt gccacaatg ctgccttttg      240
caactgcaaa gcaatgtgga atcgctgggt tggaatgttt gctaattctt ctattgggat      300
tccatattca atttccttta agaggtatca catggatcat catcggtacc ttggagctga      360
tggcgctcgat gtagatattc ctaccgattt tgagggctgg ttcttctgta ccgctttcag      420
aaagtttata tgggttattc ttcagcctct cttttatgcc ttctgacctc tgttcatcaa      480
cccaaacca attacgtatc tggaagttat caataccgtg gcacaggtca cttttgacat      540
tttaatttat tacttttttg gaattaaatc cttagtctac atgttggcag catctttact      600
tggcctgggt ttgcaccaa tttctggaca ttttatagct gagcattaca tgttcttaaa      660
gggtcatgaa acttactcat attatgggcc tctgaattta cttaccttca atgtgggtta      720
tcataatgaa catcatgatt tccccaacat tcttgaaaaa agtcttccac tggtgaggaa      780
aatagcagct gaatactatg acaacctccc tctactaat tcctggataa aagtactgta      840
tgattttgtg atggatgata caataagtcc ctactcaaga atgaagaggc accaaaaagg      900
agagatgggt ctggagtaaa tatcattagt gccaaaggga ttcttctcca aaactttaga      960
tgataaaatg gaatttttgc attattaaac ttgagaccag tgatgctcag aagctccctt     1020
ggcacaattt cagagtaaga gctcgggtgat accaagaagt gaatctggct tttaaacagt     1080
cagcctgact ctgtactgct cagtttcact cacaggaaac ttgtgacttg tgtattatcg     1140
tcattgagga tgtttcactc atgtctgtca ttttataagc atatcattta aaaagcttct     1200
aaaaagctat ttcgccagg                                     1219
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<210> 28

<211> 655

<212> DNA

<213> Homo sapiens

<400> 28

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gggccttttc ttcatagtca ggttcctgga aagcaactgg tttgtgtggg tgacacagat     120
gaaccatatt cccatgcaca ttgatcatga ccggaacatg gactggggtt ccacccagct     180
ccaggccaca tgcaatgtcc acaagtctgc cttcaatgac tggttcagtg gacacctcaa     240
cttcagatt gagcaccatc tttttccac gatgcctcga cacaattacc acaaagtggc      300
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tcccctggtg cagtccttgt gtgccaagca tggcatagag taccagtcca agcccctgct	360
gtcagccttc gccgacatca tccactcact aaaggagtca gggcagctct ggctagatgc	420
ctatcttcac caataacaac agccaccctg cccagtctgg aagaagagga ggaagactct	480
ggagccaagg cagaggggag cttgaggggac aatgccacta tagtttaata ctcagagggg	540
gttggggtttg gggacataaa gcctctgact caaactcctc ccttttatct tctagccaca	600
gttctaagac ccaaagtggg ggggtggacac agaagtcctt aggaggggaag gagct	655

<210> 29
 <211> 304
 <212> DNA
 <213> Homo sapiens

<400> 29	
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tctcaggccc aagctggatg gctgcaacat gattatggcc acctgtctgt ctacagaaaa	120
cccaagtgga accaccttgt ccacaaattc gtcattggcc acttaaaggg tgcctctgcc	180
aactggtgga atcatcgcca cttccagcac cagccaagc ctaacatctt ccacaaggat	240
cccgatgtga acatgctgca cgtgtttgtt ctgggcgaat ggcagcccat cgagtacggc	300
aaga	304

<210> 30
 <211> 918
 <212> DNA
 <213> Homo sapiens

<400> 30	
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gagcgggtggc tagtgatcga ccgtaagggtg tacaacatca gcgagttcac ccgcccgcac	120
ccaggggggt cccgggtcat cagccactac gccgggcagg atgccacgga tcccttttgt	180
gccttcaca tcaacaaggg ccttgtgaag aagtatatga actctctcct gattggagaa	240
ctgtctccag agcagcccag ctttgagccc accaagaata aagagctgac agatgagttc	300
cgggagctgc gggccacagt ggagcggatg gggctcatga aggccaacca tgtcttcttc	360
ctgctgtacc tgctgcacat cttgctgctg gatggtgcag cctggctcac cctttgggtc	420
tttgggacgt cctttttgcc cttcctctc tgtgcggtgc tgctcagtgc agttcaggcc	480
caggctgggt ggctgcagca tgactttggg cacctgtcgg tcttcagcac ctcaaagtgg	540
aaccatctgc tacatcattt tgtgattggc cacctgaagg gggccccgc cagttggtgg	600
aaccacatgc acttcagca ccattgccaag cccaactgct tccgcaaaga cccagacatc	660

aacatgcac	ccttcttctt	tgcttgggg	aagatcctct	ctgtggagct	tggaacag	720
aagaaaaaat	atatgccgta	caaccaccag	cacaratact	tcttccta	tgggcccca	780
gccttgctgc	ctctctactt	ccagtgggat	atcttctatt	ttgttatcca	gcgaaagaag	840
tgggtggact	tggcctggat	cagcaaacag	gaatacga	aagccgggct	tccattgtcc	900
accgcaaatg	cttctaaa					918

<210> 31
 <211> 1686
 <212> DNA
 <213> Homo sapiens

<400> 31						
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agcctaacat	cttcacaa	gatcccgatg	tgaacatgct	gcacgtgttt	gttctggg	120
aatggcagcc	catcgagtac	ggcaagaaga	agctgaaata	cctgccctac	aatcaccagc	180
acgaatactt	cttctgatt	gggccgccgc	tgctcatccc	catgtatttc	cagtaccaga	240
tcatcatgac	catgatcg	cataagaact	gggtggacct	ggcctggg	gtcagctact	300
acatccggtt	cttcatcacc	tacatccctt	tctacggcat	cctgggagcc	ctcttttcc	360
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tcgtcatgga	gattgaccag	gaggcctacc	gtgactgggt	cagtagccag	ctgacagcca	480
cctgcaacgt	ggagcagtc	ttcttcaacg	actgggttcag	tggaacacct	aacttccaga	540
ttgagcacca	ctcttcccc	accatgcccc	ggcacaactt	acacaagatc	gccccgctgg	600
tgaagtctct	atgtgccaa	catggcattg	aataccagga	gaagccgcta	ctgagggccc	660
tgctggacat	catcaggctc	ctgaagaagt	ctgggaagct	gtggctggac	gcctaccttc	720
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cggaccccat	gttggatctt	tctccctttc	tcctctcctt	tttctcttca	catctcccc	900
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cctgtgagtc	tccccttgca	gcctggtcac	taggcacac	ccccgctttg	gttcttcaga	1140
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tccagggccc caggcccgcg ggcacagcca gcccaaacct tgggccctgg aagagtcctc	1380
caccccatca ctagagtgtc ctgaccctgg gctttcacgg gcccattcc accgcctccc	1440
caacttgagc ctgtgacctt gggaccaaag ggggagtccc tcgtctcttg tgactcagca	1500
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cttttcctca ggggtgtcctg aggtccaaga ttctggagca atctgacct tctccaaagg	1620
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gcctg	1686

<210> 32
 <211> 1843
 <212> DNA
 <213> Homo sapiens

<400> 32	
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cccaagtgga accaccttgt ccacaaatc gtcattggcc acttaaaggg tgctctgccc	180
aactggtgga atcatcgcca ctccagcac cagccaagc ctaacatctt ccacaaggat	240
cccgatgtga acatgctgca cgtgtttgtt ctgggcgaat ggcagcccat cgagtacggc	300
aagaagaagc tgaaatacct gccctacaat caccagcacg aatacttctt cctgattggg	360
ccgccgctgc tcatcccat gtatttccag taccagatca tcatgaccat gatcgtccat	420
aagaactggg tggacctggc ctgggcgctc agctactaca tccggttctt catcacctac	480
atccctttct acggcatcct gggagccctc cttttcctca acttcacag gttcctggag	540
agccactggg ttgtgtgggt cacacagatg aatcacatcg tcatggagat tgaccaggag	600
gcctaccgtg actggttcag tagccagctg acagccacct gcaacgtgga gcagtccttc	660
ttcaacgact ggttcagtgg acaccttaac ttccagattg agcaccacct ctccccacc	720
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ggcattgaat accaggagaa gccgctactg agggccctgc tggacatcat caggctccctg	840
aagaagtctg ggaagctgtg gctggacgcc taccttcaca aatgaagcca cagcccccg	900
gacaccgtgg ggaaggggtg caggtggggt gatggccaga ggaatgatgg gcttttgttc	960
tgaggggtgt ccgagaggct ggtgtatgca ctgctcacgg accccatgtt ggatctttct	1020
ccctttctcc tctccttttt ctcttcacat ctccccata gcacctgcc ctcatgggac	1080
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ctaaagatgg gaggagacca gcggtccatg ggtctggcct gtgagtctcc ccttgcagcc	1260
tggctactag gcatcacccc cgcttttggtt cttcagatgc tcttgggggtt cataggggca	1320
ggtcctagtc gggcagggcc cctgaccctc ccggcctggc ttcactctcc ctgacggctg	1380
ccattggtcc accctttcat agagaggcct gctttgttac aaagctcggg tctccctcct	1440
gcagctcggg taagtaccgg aggcctctct taagatgtcc agggccccag gccgcggggc	1500
acagccagcc caaaccttgg gccctggaag agtcctccac cccatcacta gagtgtcttg	1560
accctgggct ttcacgggccc ccattccacc gcctcccaa cttgagcctg tgaccttggg	1620
accaaagggg gagtccctcg tctcttgtga ctcagcagag gcagtggcca cgttcaggga	1680
ggggccggct ggccctggagg ctcagcccac cctccagctt ttcctcaggg tgtcctgagg	1740
tccaagattc tggagcaatc tgacccttct ccaaaggctc tgttatcagc tgggcagtgc	1800
cagccaatcc ctggccattt ggccccaggg gacgtggggc ctg	1843

<210> 33
 <211> 2257
 <212> DNA
 <213> Homo sapiens

<400> 33	
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gagcgggtgg tagtgatcga ccgtaagggtg tacaacatca gcgagttcac ccgcgggcat	120
ccaggggggt cccgggtcat cagccactac gccgggcagg atgccacgga tccctttgtg	180
gccttccaca tcaacaaggg ccttgtgaag aagtatatga actctctcct gatttgagaa	240
ctgtctccag agcagcccag ctttgagccc accaagaata aagagctgac agatgagttc	300
cgggagctgc gggccacagt ggagcggatg gggctcatga aggccaaacca tgtcttcttc	360
ctgctgtacc tgctgcacat cttgctgctg gatgggtgcag cctgggtcac cctttgggtc	420
tttgggacgt cttttttgcc cttcctctc tgtgcggtgc tgctcagtgc agttcagcag	480
gcccagctg gatggctgca acatgattat ggccacctgt ctgtctacag aaaacccaag	540
tggaaccacc ttgtccacaa attcgtcatt ggccacttaa agggtgccctc tgccaactgg	600
tggaatcatc gccacttcca gcaccacgcc aagcctaaca tcttccacaa ggatcccgat	660
gtgaacatgc tgcacgtggt tgttctgggc gaatggcagc ccatcgagta cggcaagaag	720
aagctgaaat acctgcccta caatcaccag cacgaatact tcttctgat tgggcgcggc	780
ctgctcatcc ccatgtattt ccagtaccag atcatcatga ccatgatcgt ccataagaac	840
tgggtggacc tggcctgggc cgtcagctac tacatccggt tcttcatcac ctacatccct	900
ttctacggca tcttgggagc cctccttttc ctcaacttca tcaggttctt ggagagccac	960

tggtttgtgt	gggtcacaca	gatgaatcac	atcgatcatgg	agattgacca	ggaggcctac	1020
cgtgactggt	tcagtagcca	gctgacagcc	acctgcaacg	tggagcagtc	cttcttcaac	1080
gactgggttca	gtggacacct	taacttccag	attgagcacc	acctcttccc	caccatgccc	1140
cggcacaact	tacacaagat	cgccccgctg	gtgaagtctc	tatgtgcca	gcatggcatt	1200
gaataccagg	agaagccgct	actgagggcc	ctgctggaca	tcacaggtc	cctgaagaag	1260
tctgggaagc	tgtggctgga	cgcctacctt	cacaaatgaa	gccacagccc	ccgggacacc	1320
gtggggaagg	ggtgcagggtg	gggtgatggc	cagaggaatg	atgggctttt	gttctgaggg	1380
gtgtccgaga	ggctggtgta	tgcactgctc	acggacceca	tgttgatct	ttctcccttt	1440
ctcctctcct	ttttctcttc	acatctcccc	catagcacc	tgcctcatg	ggacctgccc	1500
tcctcagcc	gtcagccatc	agccatggcc	ctcccagtc	ctcctagccc	cttcttccaa	1560
ggagcagaga	ggtggccacc	gggggtggct	ctgtcctacc	tccactctct	gcccctaaag	1620
atgggaggag	accagcggtc	catgggtctg	gcctgtgagt	ctccccttgc	agcctggtea	1680
ctaggcatca	ccccgccttt	ggttcttcag	atgctcttgg	ggttcatagg	ggcaggctct	1740
agtcgggcag	ggccccctgac	cctcccggcc	tggcttcaact	ctccctgacg	gctgccattg	1800
gtccaccctt	tcatagagag	gcctgctttg	ttacaaagct	cgggtctccc	tctgcagct	1860
cggttaagta	cccaggccct	ctcttaagat	gtccagggcc	ccaggccccgc	gggcacagcc	1920
agcccaaacc	ttgggccctg	gaagagtctt	ccaccccatc	actagagtgc	tctgaccctg	1980
ggctttcacg	ggccccattc	caccgcctcc	ccaacttgag	cctgtgacct	tgggacaaaa	2040
gggggagtc	ctcgtctctt	gtgactcagc	agaggcagtg	gccacgttca	gggaggggccc	2100
ggctggcctg	gaggetcagc	ccaccctcca	gcttttctct	aggggtgtct	gaggtccaag	2160
attctggagc	aatctgaccc	ttctccaaag	gctctgttat	cagctgggca	gtgccagcca	2220
atccctggcc	atttgcccc	aggggacgtg	ggccctg			2257

<210> 34

<211> 406

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> (1)..(406)

<223> Amino acids 306,329,331,334,358,375,and 382 uncertain of sequence

<400> 34

His	Ala	Asp	Arg	Arg	Arg	Glu	Ile	Leu	Ala	Lys	Tyr	Pro	Glu	Ile	Lys
1				5					10					15	

Ser Leu Met Lys Pro Asp Pro Asn Leu Ile Trp Ile Ile Ile Met Met
 20 25 30
 Val Leu Thr Gln Leu Gly Ala Phe Tyr Ile Val Lys Asp Leu Asp Trp
 35 40 45
 Lys Trp Val Ile Phe Gly Ala Tyr Ala Phe Gly Ser Cys Ile Asn His
 50 55 60
 Ser Met Thr Leu Ala Ile His Glu Ile Ala His Asn Ala Ala Phe Gly
 65 70 75 80
 Asn Cys Lys Ala Met Trp Asn Arg Trp Phe Gly Met Phe Ala Asn Leu
 85 90 95
 Pro Ile Gly Ile Pro Tyr Ser Ile Ser Phe Lys Arg Tyr His Met Asp
 100 105 110
 His His Arg Tyr Leu Gly Ala Asp Gly Val Asp Val Asp Ile Pro Thr
 115 120 125
 Asp Phe Glu Gly Trp Phe Phe Cys Thr Ala Phe Arg Lys Phe Ile Trp
 130 135 140
 Val Ile Leu Gln Pro Leu Phe Tyr Ala Phe Arg Pro Leu Phe Ile Asn
 145 150 155 160
 Pro Lys Pro Ile Thr Tyr Leu Glu Val Ile Asn Thr Val Ala Gln Val
 165 170 175
 Thr Phe Asp Ile Leu Ile Tyr Tyr Phe Leu Gly Ile Lys Ser Leu Val
 180 185 190
 Tyr Met Leu Ala Ala Ser Leu Leu Gly Leu Gly Leu His Pro Ile Ser
 195 200 205
 Gly His Phe Ile Ala Glu His Tyr Met Phe Leu Lys Gly His Glu Thr
 210 215 220
 Tyr Ser Tyr Tyr Gly Pro Leu Asn Leu Leu Thr Phe Asn Val Gly Tyr
 225 230 235 240
 His Asn Glu His His Asp Phe Pro Asn Ile Pro Gly Lys Ser Leu Pro
 245 250 255
 Leu Val Arg Lys Ile Ala Ala Glu Tyr Tyr Asp Asn Leu Pro His Tyr
 260 265 270
 Asn Ser Trp Ile Lys Val Leu Tyr Asp Phe Val Met Asp Asp Thr Ile
 275 280 285
 Ser Pro Tyr Ser Arg Met Lys Arg His Gln Lys Gly Glu Met Val Leu
 290 295 300
 Glu Xaa Ile Ser Leu Val Pro Lys Gly Phe Phe Ser Lys Thr Leu Asp
 305 310 315 320
 Asp Lys Met Glu Phe Leu His Tyr Xaa Thr Xaa Asp Gln Xaa Cys Ser
 325 330 335
 Glu Ala Pro Leu Ala Gln Phe Gln Ser Lys Ser Ser Val Ile Pro Arg

340	345	350
Ser Glu Ser Gly Phe Xaa Thr Val Ser Leu Thr Leu Tyr Cys Ser Val		
355	360	365
Ser Leu Thr Gly Asn Leu Xaa Leu Val Tyr Tyr Arg His Xaa Gly Cys		
370	375	380
Phe Thr His Val Cys His Phe Ile Ser Ile Ser Phe Lys Lys Leu Leu		
385	390	395
Lys Ser Tyr Phe Ala Arg		
405		

<210> 35
 <211> 218
 <212> PRT
 <213> Homo sapiens

 <220>
 <221> UNSURE
 <222> (1)..(218)
 <223> Amino acids 145,168,174,186,189,198, and 202 uncertain of sequence

<400> 35

Tyr Leu Leu Arg Pro Leu Leu Pro His Leu Cys Ala Thr Ile Gly Ala		
1	5	10
Glu Ser Phe Leu Gly Leu Phe Phe Ile Val Arg Phe Leu Glu Ser Asn		
20	25	30
Trp Phe Val Trp Val Thr Gln Met Asn His Ile Pro Met His Ile Asp		
35	40	45
His Asp Arg Asn Met Asp Trp Val Ser Thr Gln Leu Gln Ala Thr Cys		
50	55	60
Asn Val His Lys Ser Ala Phe Asn Asp Trp Phe Ser Gly His Leu Asn		
65	70	75
Phe Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Tyr		
85	90	95
His Lys Val Ala Pro Leu Val Gln Ser Leu Cys Ala Lys His Gly Ile		
100	105	110
Glu Tyr Gln Ser Lys Pro Leu Leu Ser Ala Phe Ala Asp Ile Ile His		
115	120	125
Ser Leu Lys Glu Ser Gly Gln Leu Trp Leu Asp Ala Tyr Leu His Gln		
130	135	140
Xaa Gln Gln Pro Pro Cys Pro Val Trp Lys Lys Arg Arg Lys Thr Leu		
145	150	155
Glu Pro Arg Gln Arg Gly Ala Xaa Gly Thr Met Pro Leu Xaa Phe Asn		
165	170	175

Thr Gln Arg Gly Leu Gly Leu Gly Thr Xaa Ser Leu Xaa Leu Lys Leu
180 185 190

Leu Pro Phe Ile Phe Xaa Pro Gln Phe Xaa Asp Pro Lys Trp Gly Val
195 200 205

Asp Thr Glu Val Pro Arg Arg Glu Gly Ala
210 215

<210> 36

<211> 87

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> (1)..(87)

<223> Amino acid 87 uncertain of sequence

<400> 36

Val Phe Tyr Phe Gly Asn Gly Trp Ile Pro Thr Leu Ile Thr Ala Phe
1 5 10 15

Val Leu Ala Thr Ser Gln Ala Gln Ala Gly Trp Leu Gln His Asp Tyr
20 25 30

Gly His Leu Ser Val Tyr Arg Lys Pro Lys Trp Asn His Leu Val His
35 40 45

Lys Phe Val Ile Gly His Leu Lys Gly Ala Ser Ala Asn Trp Trp Asn
50 55 60

His Arg His Phe Gln His His Ala Lys Pro Asn Leu Gly Glu Trp Gln
65 70 75 80

Pro Ile Glu Tyr Gly Lys Xaa
85

<210> 37

<211> 306

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> (1)..(306)

<223> Amino acid 252 uncertain of sequence

<400> 37

Gln Gly Pro Thr Pro Arg Tyr Phe Thr Trp Asp Glu Val Ala Gln Arg
1 5 10 15

Ser Gly Cys Glu Glu Arg Trp Leu Val Ile Asp Arg Lys Val Tyr Asn
20 25 30

Ile Ser Glu Phe Thr Arg Arg His Pro Gly Gly Ser Arg Val Ile Ser

35

40

45

His Tyr Ala Gly Gln Asp Ala Thr Asp Pro Phe Val Ala Phe His Ile
 50 55 60
 Asn Lys Gly Leu Val Lys Lys Tyr Met Asn Ser Leu Leu Ile Gly Glu
 65 70 75 80
 Leu Ser Pro Glu Gln Pro Ser Phe Glu Pro Thr Lys Asn Lys Glu Leu
 85 90 95
 Thr Asp Glu Phe Arg Glu Leu Arg Ala Thr Val Glu Arg Met Gly Leu
 100 105 110
 Met Lys Ala Asn His Val Phe Phe Leu Leu Tyr Leu Leu His Ile Leu
 115 120 125
 Leu Leu Asp Gly Ala Ala Trp Leu Thr Leu Trp Val Phe Gly Thr Ser
 130 135 140
 Phe Leu Pro Phe Leu Leu Cys Ala Val Leu Leu Ser Ala Val Gln Ala
 145 150 155 160
 Gln Ala Gly Trp Leu Gln His Asp Phe Gly His Leu Ser Val Phe Ser
 165 170 175
 Thr Ser Lys Trp Asn His Leu Leu His His Phe Val Ile Gly His Leu
 180 185 190
 Lys Gly Ala Pro Ala Ser Trp Trp Asn His Met His Phe Gln His His
 195 200 205
 Ala Lys Pro Asn Cys Phe Arg Lys Asp Pro Asp Ile Asn Met His Pro
 210 215 220
 Phe Phe Phe Ala Leu Gly Lys Ile Leu Ser Val Glu Leu Gly Lys Gln
 225 230 235 240
 Lys Lys Lys Tyr Met Pro Tyr Asn His Gln His Xaa Tyr Phe Phe Leu
 245 250 255
 Ile Gly Pro Pro Ala Leu Leu Pro Leu Tyr Phe Gln Trp Tyr Ile Phe
 260 265 270
 Tyr Phe Val Ile Gln Arg Lys Lys Trp Val Asp Leu Ala Trp Ile Ser
 275 280 285
 Lys Gln Glu Tyr Asp Glu Ala Gly Leu Pro Leu Ser Thr Ala Asn Ala
 290 295 300

Ser Lys
305

<210> 38
 <211> 562
 <212> PRT
 <213> Homo sapiens

<220>
 <221> UNSURE
 <222> (1)..(562)

<223> Amino acids 242,268,405,438,464,482,497, and 562 uncertain of sequence

<400> 38

His	Leu	Lys	Gly	Ala	Ser	Ala	Asn	Trp	Trp	Asn	His	Arg	His	Phe	Gln
1				5					10					15	
His	His	Ala	Lys	Pro	Asn	Ile	Phe	His	Lys	Asp	Pro	Asp	Val	Asn	Met
			20					25					30		
Leu	His	Val	Phe	Val	Leu	Gly	Glu	Trp	Gln	Pro	Ile	Glu	Tyr	Gly	Lys
		35					40					45			
Lys	Lys	Leu	Lys	Tyr	Leu	Pro	Tyr	Asn	His	Gln	His	Glu	Tyr	Phe	Phe
	50					55					60				
Leu	Ile	Gly	Pro	Pro	Leu	Leu	Ile	Pro	Met	Tyr	Phe	Gln	Tyr	Gln	Ile
65					70					75					80
Ile	Met	Thr	Met	Ile	Val	His	Lys	Asn	Trp	Val	Asp	Leu	Ala	Trp	Ala
				85					90					95	
Val	Ser	Tyr	Tyr	Ile	Arg	Phe	Phe	Ile	Thr	Tyr	Ile	Pro	Phe	Tyr	Gly
			100					105					110		
Ile	Leu	Gly	Ala	Leu	Leu	Phe	Leu	Asn	Phe	Ile	Arg	Phe	Leu	Glu	Ser
		115					120					125			
His	Trp	Phe	Val	Trp	Val	Thr	Gln	Met	Asn	His	Ile	Val	Met	Glu	Ile
	130					135					140				
Asp	Gln	Glu	Ala	Tyr	Arg	Asp	Trp	Phe	Ser	Ser	Gln	Leu	Thr	Ala	Thr
145					150					155					160
Cys	Asn	Val	Glu	Gln	Ser	Phe	Phe	Asn	Asp	Trp	Phe	Ser	Gly	His	Leu
				165					170					175	
Asn	Phe	Gln	Ile	Glu	His	His	Leu	Phe	Pro	Thr	Met	Pro	Arg	His	Asn
		180						185					190		
Leu	His	Lys	Ile	Ala	Pro	Leu	Val	Lys	Ser	Leu	Cys	Ala	Lys	His	Gly
		195					200					205			
Ile	Glu	Tyr	Gln	Glu	Lys	Pro	Leu	Leu	Arg	Ala	Leu	Leu	Asp	Ile	Ile
	210					215						220			
Arg	Ser	Leu	Lys	Lys	Ser	Gly	Lys	Leu	Trp	Leu	Asp	Ala	Tyr	Leu	His
225					230					235					240
Lys	Xaa	Ser	His	Ser	Pro	Arg	Asp	Thr	Val	Gly	Lys	Gly	Cys	Arg	Trp
				245					250					255	
Gly	Asp	Gly	Gln	Arg	Asn	Asp	Gly	Leu	Leu	Phe	Xaa	Gly	Val	Ser	Glu
			260					265					270		
Arg	Leu	Val	Tyr	Ala	Leu	Leu	Thr	Asp	Pro	Met	Leu	Asp	Leu	Ser	Pro
		275					280					285			
Phe	Leu	Leu	Ser	Phe	Phe	Ser	Ser	His	Leu	Pro	His	Ser	Thr	Leu	Pro

290	295	300
Ser Trp Asp Leu Pro	Ser Leu Ser Arg Gln	Pro Ser Ala Met Ala Leu
305	310	315 320
Pro Val Pro Pro Ser	Pro Phe Phe Gln Gly	Ala Glu Arg Trp Pro Pro
	325	330 335
Gly Val Ala Leu Ser	Tyr Leu His Ser	Leu Pro Leu Lys Met Gly Gly
	340	345 350
Asp Gln Arg Ser Met	Gly Leu Ala Cys Glu	Ser Pro Leu Ala Ala Trp
	355	360 365
Ser Leu Gly Ile Thr	Pro Ala Leu Val Leu	Gln Met Leu Leu Gly Phe
	370	375 380
Ile Gly Ala Gly Pro	Ser Arg Ala Gly Pro	Leu Thr Leu Pro Ala Trp
385	390	395 400
Leu His Ser Pro Xaa	Arg Leu Pro Leu Val	His Pro Phe Ile Glu Arg
	405	410 415
Pro Ala Leu Leu Gln	Ser Ser Gly Leu Pro	Pro Ala Ala Arg Leu Ser
	420	425 430
Thr Arg Gly Leu Ser	Xaa Asp Val Gln Gly	Pro Arg Pro Ala Gly Thr
	435	440 445
Ala Ser Pro Asn Leu	Gly Pro Trp Lys Ser	Pro Pro His His Xaa
450	455	460
Ser Ala Leu Thr Leu	Gly Phe His Gly Pro	His Ser Thr Ala Ser Pro
465	470	475 480
Thr Xaa Ala Cys Asp	Leu Gly Thr Lys Gly	Gly Val Pro Arg Leu Leu
	485	490 495
Xaa Leu Ser Arg Gly	Ser Gly His Val Gln	Gly Gly Ala Gly Trp Pro
	500	505 510
Gly Gly Ser Ala His	Pro Pro Ala Phe Pro	Gln Gly Val Leu Arg Ser
	515	520 525
Lys Ile Leu Glu Gln	Ser Asp Pro Ser Pro	Lys Ala Leu Leu Ser Ala
	530	535 540
Gly Gln Cys Gln Pro	Ile Pro Gly His Leu	Ala Pro Gly Asp Val Gly
545	550	555 560

Pro Xaa

<210> 39
 <211> 615
 <212> PRT
 <213> Homo sapiens

 <220>
 <221> UNSURE
 <222> (1)..(615)

<223> Amino acids 295,321,458,491,517,535,550, and 615 uncertain of sequence

<400> 39

Val Phe Tyr Phe Gly Asn Gly Trp Ile Pro Thr Leu Ile Thr Ala Phe
1 5 10 15

Val Leu Ala Thr Ser Gln Ala Gln Ala Gly Trp Leu Gln His Asp Tyr
20 25 30

Gly His Leu Ser Val Tyr Arg Lys Pro Lys Trp Asn His Leu Val His
35 40 45

Lys Phe Val Ile Gly His Leu Lys Gly Ala Ser Ala Asn Trp Trp Asn
50 55 60

His Arg His Phe Gln His His Ala Lys Pro Asn Ile Phe His Lys Asp
65 70 75 80

Pro Asp Val Asn Met Leu His Val Phe Val Leu Gly Glu Trp Gln Pro
85 90 95

Ile Glu Tyr Gly Lys Lys Lys Leu Lys Tyr Leu Pro Tyr Asn His Gln
100 105 110

His Glu Tyr Phe Phe Leu Ile Gly Pro Pro Leu Leu Ile Pro Met Tyr
115 120 125

Phe Gln Tyr Gln Ile Ile Met Thr Met Ile Val His Lys Asn Trp Val
130 135 140

Asp Leu Ala Trp Ala Val Ser Tyr Tyr Ile Arg Phe Phe Ile Thr Tyr
145 150 155 160

Ile Pro Phe Tyr Gly Ile Leu Gly Ala Leu Leu Phe Leu Asn Phe Ile
165 170 175

Arg Phe Leu Glu Ser His Trp Phe Val Trp Val Thr Gln Met Asn His
180 185 190

Ile Val Met Glu Ile Asp Gln Glu Ala Tyr Arg Asp Trp Phe Ser Ser
195 200 205

Gln Leu Thr Ala Thr Cys Asn Val Glu Gln Ser Phe Phe Asn Asp Trp
210 215 220

Phe Ser Gly His Leu Asn Phe Gln Ile Glu His His Leu Phe Pro Thr
225 230 235 240

Met Pro Arg His Asn Leu His Lys Ile Ala Pro Leu Val Lys Ser Leu
245 250 255

Cys Ala Lys His Gly Ile Glu Tyr Gln Glu Lys Pro Leu Leu Arg Ala
260 265 270

Leu Leu Asp Ile Ile Arg Ser Leu Lys Lys Ser Gly Lys Leu Trp Leu
275 280 285

Asp Ala Tyr Leu His Lys Xaa Ser His Ser Pro Arg Asp Thr Val Gly

290	295	300
Lys Gly Cys Arg Trp 305	Gly Asp Gly Gln Arg 310	Asn Asp Gly Leu Leu Phe 315 320
Xaa Gly Val Ser 325	Glu Arg Leu Val Tyr 330	Ala Leu Leu Thr Asp Pro Met 335
Leu Asp Leu Ser 340	Pro Phe Leu Leu Ser 345	Phe Phe Ser Ser His Leu Pro 350
His Ser Thr Leu Pro Ser 355	Trp Asp Leu Pro Ser 360	Leu Ser Arg Gln Pro 365
Ser Ala Met Ala Leu Pro 370	Val Pro Pro Ser Pro 375	Phe Phe Gln Gly Ala 380
Glu Arg Trp Pro Pro 385	Gly Val Ala Leu Ser 390	Tyr Leu His Ser Leu Pro 395 400
Leu Lys Met Gly 405	Gly Asp Gln Arg Ser 410	Met Gly Leu Ala Cys Glu Ser 415
Pro Leu Ala Ala Trp 420	Ser Leu Gly Ile Thr 425	Pro Ala Leu Val Leu Gln 430
Met Leu Leu Gly Phe Ile 435	Gly Ala Gly Pro Ser 440	Arg Ala Gly Pro Leu 445
Thr Leu Pro Ala Trp 450	Leu His Ser Pro Xaa 455	Arg Leu Pro Leu Val His 460
Pro Phe Ile Glu Arg 465	Pro Ala Leu Leu Gln 470	Ser Ser Gly Leu Pro Pro 475 480
Ala Ala Arg Leu Ser 485	Thr Arg Gly Leu Ser 490	Xaa Asp Val Gln Gly Pro 495
Arg Pro Ala Gly Thr 500	Ala Ser Pro Asn Leu 505	Gly Pro Trp Lys Ser Pro 510
Pro Pro His His Xaa Ser 515	Ala Leu Thr Leu Gly 520	Phe His Gly Pro His 525
Ser Thr Ala Ser Pro Thr 530	Xaa Ala Cys Asp Leu 535	Gly Thr Lys Gly Gly 540
Val Pro Arg Leu Leu 545	Xaa Leu Ser Arg Gly 550	Ser Gly His Val Gln Gly 555 560
Gly Ala Gly Trp Pro 565	Gly Gly Ser Ala His 570	Pro Pro Ala Phe Pro Gln 575
Gly Val Leu Arg Ser Lys 580	Ile Leu Glu Gln Ser 585	Asp Pro Ser Pro Lys 590
Ala Leu Leu Ser Ala Gly 595	Gln Cys Gln Pro Ile 600	Pro Gly His Leu Ala 605
Pro Gly Asp Val Gly Pro 610	Xaa 615	

<210> 40
 <211> 753
 <212> PRT
 <213> Homo sapiens

<220>
 <221> UNSURE
 <222> (1)..(753)
 <223> Amino acids 433,459,596,629,655,673,688, and 753 uncertain of sequence

<400> 40

Gln	Gly	Pro	Thr	Pro	Arg	Tyr	Phe	Thr	Trp	Asp	Glu	Val	Ala	Gln	Arg	1	5	10	15
Ser	Gly	Cys	Glu	Glu	Arg	Trp	Leu	Val	Ile	Asp	Arg	Lys	Val	Tyr	Asn	20	25	30	
Ile	Ser	Glu	Phe	Thr	Arg	Arg	His	Pro	Gly	Gly	Ser	Arg	Val	Ile	Ser	35	40	45	
His	Tyr	Ala	Gly	Gln	Asp	Ala	Thr	Asp	Pro	Phe	Val	Ala	Phe	His	Ile	50	55	60	
Asn	Lys	Gly	Leu	Val	Lys	Lys	Tyr	Met	Asn	Ser	Leu	Leu	Ile	Gly	Glu	65	70	75	80
Leu	Ser	Pro	Glu	Gln	Pro	Ser	Phe	Glu	Pro	Thr	Lys	Asn	Lys	Glu	Leu	85	90	95	
Thr	Asp	Glu	Phe	Arg	Glu	Leu	Arg	Ala	Thr	Val	Glu	Arg	Met	Gly	Leu	100	105	110	
Met	Lys	Ala	Asn	His	Val	Phe	Phe	Leu	Leu	Tyr	Leu	Leu	His	Ile	Leu	115	120	125	
Leu	Leu	Asp	Gly	Ala	Ala	Trp	Leu	Thr	Leu	Trp	Val	Phe	Gly	Thr	Ser	130	135	140	
Phe	Leu	Pro	Phe	Leu	Leu	Cys	Ala	Val	Leu	Leu	Ser	Ala	Val	Gln	Gln	145	150	155	160
Ala	Gln	Ala	Gly	Trp	Leu	Gln	His	Asp	Tyr	Gly	His	Leu	Ser	Val	Tyr	165	170	175	
Arg	Lys	Pro	Lys	Trp	Asn	His	Leu	Val	His	Lys	Phe	Val	Ile	Gly	His	180	185	190	
Leu	Lys	Gly	Ala	Ser	Ala	Asn	Trp	Trp	Asn	His	Arg	His	Phe	Gln	His	195	200	205	
His	Ala	Lys	Pro	Asn	Ile	Phe	His	Lys	Asp	Pro	Asp	Val	Asn	Met	Leu	210	215	220	
His	Val	Phe	Val	Leu	Gly	Glu	Trp	Gln	Pro	Ile	Glu	Tyr	Gly	Lys	Lys	225	230	235	240
Lys	Leu	Lys	Tyr	Leu	Pro	Tyr	Asn	His	Gln	His	Glu	Tyr	Phe	Phe	Leu	245	250	255	

Ile Gly Pro Pro Leu Leu Ile Pro Met Tyr Phe Gln Tyr Gln Ile Ile
 260 265 270
 Met Thr Met Ile Val His Lys Asn Trp Val Asp Leu Ala Trp Ala Val
 275 280 285
 Ser Tyr Tyr Ile Arg Phe Phe Ile Thr Tyr Ile Pro Phe Tyr Gly Ile
 290 295 300
 Leu Gly Ala Leu Leu Phe Leu Asn Phe Ile Arg Phe Leu Glu Ser His
 305 310 315 320
 Trp Phe Val Trp Val Thr Gln Met Asn His Ile Val Met Glu Ile Asp
 325 330 335
 Gln Glu Ala Tyr Arg Asp Trp Phe Ser Ser Gln Leu Thr Ala Thr Cys
 340 345 350
 Asn Val Glu Gln Ser Phe Phe Asn Asp Trp Phe Ser Gly His Leu Asn
 355 360 365
 Phe Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu
 370 375 380
 His Lys Ile Ala Pro Leu Val Lys Ser Leu Cys Ala Lys His Gly Ile
 385 390 395 400
 Glu Tyr Gln Glu Lys Pro Leu Leu Arg Ala Leu Leu Asp Ile Ile Arg
 405 410 415
 Ser Leu Lys Lys Ser Gly Lys Leu Trp Leu Asp Ala Tyr Leu His Lys
 420 425 430
 Xaa Ser His Ser Pro Arg Asp Thr Val Gly Lys Gly Cys Arg Trp Gly
 435 440 445
 Asp Gly Gln Arg Asn Asp Gly Leu Leu Phe Xaa Gly Val Ser Glu Arg
 450 455 460
 Leu Val Tyr Ala Leu Leu Thr Asp Pro Met Leu Asp Leu Ser Pro Phe
 465 470 475 480
 Leu Leu Ser Phe Phe Ser Ser His Leu Pro His Ser Thr Leu Pro Ser
 485 490 495
 Trp Asp Leu Pro Ser Leu Ser Arg Gln Pro Ser Ala Met Ala Leu Pro
 500 505 510
 Val Pro Pro Ser Pro Phe Phe Gln Gly Ala Glu Arg Trp Pro Pro Gly
 515 520 525
 Val Ala Leu Ser Tyr Leu His Ser Leu Pro Leu Lys Met Gly Gly Asp
 530 535 540
 Gln Arg Ser Met Gly Leu Ala Cys Glu Ser Pro Leu Ala Ala Trp Ser
 545 550 555 560
 Leu Gly Ile Thr Pro Ala Leu Val Leu Gln Met Leu Leu Gly Phe Ile
 565 570 575

Gly Ala Gly Pro Ser Arg Ala Gly Pro Leu Thr Leu Pro Ala Trp Leu
580 585 590

His Ser Pro Xaa Arg Leu Pro Leu Val His Pro Phe Ile Glu Arg Pro
595 600 605

Ala Leu Leu Gln Ser Ser Gly Leu Pro Pro Ala Ala Arg Leu Ser Thr
610 615 620

Arg Gly Leu Ser Xaa Asp Val Gln Gly Pro Arg Pro Ala Gly Thr Ala
625 630 635 640

Ser Pro Asn Leu Gly Pro Trp Lys Ser Pro Pro Pro His His Xaa Ser
645 650 655

Ala Leu Thr Leu Gly Phe His Gly Pro His Ser Thr Ala Ser Pro Thr
660 665 670

Xaa Ala Cys Asp Leu Gly Thr Lys Gly Gly Val Pro Arg Leu Leu Xaa
675 680 685

Leu Ser Arg Gly Ser Gly His Val Gln Gly Gly Ala Gly Trp Pro Gly
690 695 700

Gly Ser Ala His Pro Pro Ala Phe Pro Gln Gly Val Leu Arg Ser Lys
705 710 715 720

Ile Leu Glu Gln Ser Asp Pro Ser Pro Lys Ala Leu Leu Ser Ala Gly
725 730 735

Gln Cys Gln Pro Ile Pro Gly His Leu Ala Pro Gly Asp Val Gly Pro
740 745 750

Xaa

C1
cont